

**STIC Biotechnology Systems Branch**

**RAW SEQUENCE LISTING**  
**ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/564,136  
Source: LF420  
Date Processed by STIC: 10/31/2006

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENT/IN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER:

10/564,136

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics  
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino  
Numbering The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) \_\_\_\_ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0  
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences  
(OLD RULES) Sequence(s) \_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.  
27 thru 215
- 8 Skipped Sequences  
(NEW RULES) Sequence(s) \_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9 Use of n's or Xaa's  
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>  
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)
- 11 Use of <220> Sequence(s) \_\_\_\_ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules
- 12 PatentIn 2.0  
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWO

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/564,136

DATE: 10/31/2006  
TIME: 15:10:35

Input Set : A:\10564136.RAW  
Output Set: N:\CRF4\10312006\J564136.raw

3 <110> APPLICANT: Olson-Munoz, Marilyn C.  
4 Curtis, Michelle L.  
5 Ip, Hon S.  
6 Kwiatkowski, Robert W., Jr.  
7 Armantrout, Kyle C.  
8 Cao, Feng  
9 Hurwitz, Bonnie L.  
10 Machmeier, Daniel K.  
11 Olson, Sarah M.  
12 Chehak, Anne  
14 <120> TITLE OF INVENTION: Assays for the Direct Measurement of Gene Dosage  
16 <130> FILE REFERENCE: FORS-10718  
C--> 18 <140> CURRENT APPLICATION NUMBER: US/10/564,136  
C--> 18 <141> CURRENT FILING DATE: 2006-01-10  
E--> 18 <160> NUMBER OF SEQ ID NOS: 230  
20 <170> SOFTWARE: PatentIn version 3.3

Does Not Comply  
Corrected Diskette Needed  
(pgs-1)

found 39

## ERRORED SEQUENCES

243 <210> SEQ ID NO: 26  
244 <211> LENGTH: 25  
245 <212> TYPE: DNA  
246 <213> ORGANISM: Homo sapiens  
248 <400> SEQUENCE: 26  
E--> 249 cgcgcgcgagg cctgagcaac gtgca  
E--> 362 <210> SEQ ID NO:  
E--> 362 <211> LENGTH:  
E--> 362 <212> TYPE:  
E--> 362 <213> ORGANISM:  
E--> 362 <400> SEQUENCE: 215  
363 gagattgtgc acgaggactt gaagatgggg tctgatgggg agagtgaacca ggcttcagcc 60  
365 acgtctcgg atgaggtgca gtctccagt g 91  
E--> 368 <210> SEQ ID NO: 216

25 (2)

27

Missing Sequence from 27 Thru 215.  
for Intentionally Skipped Sequences.  
Pls us this format . 210 000 } See Item 8  
400 000 } on Error  
Summary  
Sheet.

RAW SEQUENCE LISTING ERROR SUMMARY  
 PATENT APPLICATION: US/10/564,136

DATE: 10/31/2006  
 TIME: 15:10:36

Input Set : A:\10564136.RAW  
 Output Set: N:\CRF4\10312006\J564136.raw

**Invalid Line Length:**

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:26; Line(s) 249,250,251,252,253,254,255,256,257,258,259,260,261,262  
 Seq#:26; Line(s) 263,264,265,266,267,268,269,270,271,272,273,274,275,276  
 Seq#:26; Line(s) 277,278,279,280,281,282,283,284,285,286,287,288,289,290  
 Seq#:26; Line(s) 291,292,293,294,295,296,297,298,299,300,301,302,303,304  
 Seq#:26; Line(s) 305,306,307,308,309,310,311,312,313,314,315,316,317,318  
 Seq#:26; Line(s) 319,320,321,322,323,324,325,326,327,328,329,330,331,332  
 Seq#:26; Line(s) 333,334,335,336,337,338,339,340,341,342,343,344,345,346  
 Seq#:26; Line(s) 347,348,349,350,351,352,353,354,355,356,357,358,359,360  
 Seq#:26; Line(s) 361

**Skipped Sequences(NEW RULES):**

Sequence(s) \_\_missing. If intentional, please use the following format for each skipped sequence.

<210> sequence id number

<400> sequence id number

000

Seq#:27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50  
 Seq#:51,52,53,54,55,56,57,58,59,60,61,62,63,64,65,66,67,68,69,70,71,72,73,74  
 Seq#:75,76,77,78,79,80,81,82,83,84,85,86,87,88,89,90,91,92,93,94,95,96,97,98  
 Seq#:99,100,101,102,103,104,105,106,107,108,109,110,111,112,113,114,115,116  
 Seq#:117,118,119,120,121,122,123,124,125,126,127,128,129,130,131,132,133,134  
 Seq#:135,136,137,138,139,140,141,142,143,144,145,146,147,148,149,150,151,152  
 Seq#:153,154,155,156,157,158,159,160,161,162,163,164,165,166,167,168,169,170  
 Seq#:171,172,173,174,175,176,177,178,179,180,181,182,183,184,185,186,187,188  
 Seq#:189,190,191,192,193,194,195,196,197,198,199,200,201,202,203,204,205,206  
 Seq#:207,208,209,210,211,212,213,214,215

## VERIFICATION SUMMARY

DATE: 10/31/2006

PATENT APPLICATION: US/10/564,136

TIME: 15:10:36

Input Set : A:\10564136.RAW

Output Set: N:\CRF4\10312006\J564136.raw

L:18 M:270 C: Current Application Number differs, Replaced Current Application No  
L:18 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:187 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (19) SEQUENCE:  
L:249 M:254 E: No. of Bases conflict, LENGTH:Input:2 Counted:25 SEQ:26  
L:362 M:282 E: Numeric Field Identifier Missing, <210> is required.  
L:362 M:282 E: Numeric Field Identifier Missing, <211> is required.  
L:362 M:282 E: Numeric Field Identifier Missing, <212> is required.  
L:362 M:282 E: Numeric Field Identifier Missing, <213> is required.  
L:362 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:26 differs:215  
L:368 M:216 E: (34) Seq.#s missing, SEQ ID NOS: 27 thru 215  
L:18 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (230) Counted (39)